Macrocyclic Amino Carboxylates as Selective MMP-8 Inhibitors

Robert J. Cherney,* Li Wang, Dayton T. Meyer, Chu-Baio Xue, Zelda R. Wasserman, Karl D. Hardman, Patty K. Welch,[†] Maryanne B. Covington,[†] Robert A. Copeland, Elizabeth C. Arner,[†] William F. DeGrado,¹ and Carl P. Decicco

Chemical and Physical Sciences and Inflammatory Diseases Research, The DuPont Merck Pharmaceutical Co., Experimental Station, Wilmington Delaware 19880-0500

Received December 19, 1997

Matrix metalloproteinases (MMPs) are a family of zinc-containing endopeptidases needed for normal turnover and maintenance of the extracellular matrix.² Their proteolytic activity is tightly controlled by endogenous tissue inhibitors of metalloproteinases (TIMPs) and the nonspecific $\alpha 2$ -macroglobulins.³ Disruption of this balance and overproduction of the MMPs results in the degradation of the matrix, which includes cartilage and connective tissues. As a result, the MMPs have been implicated in several diseases including arthritis⁴ and tumor metastasis.⁵ Inhibition of the MMPs, therefore, has gained considerable attention and has become an important strategy in the development of novel therapeutics. However, with the large number of MMPs now characterized, the selective inhibition of the therapeutically relevant MMP(s) will be of paramount importance when considering the potential toxicity of a chronically dosed drug acting on enzymes involved in tissue turnover. We have been interested in, and have recently disclosed, the synthesis of potent carboxylates as broad⁶ and selective⁷ inhibitors of the MMPs. In an effort to improve potency, selectivity, and metabolic stability of these linear inhibitors, we investigated macrocyclic amino carboxylates linked from P1 to P2', having the general formula 1. In this communication, we describe the discovery of a novel class of macrocycles as selective MMP-8 inhibitors.

Scheme 1



Design. In a recent report,⁶ we disclosed the X-ray crystal structure of carboxylate **2** cocrystallized with MMP-3.⁸ As shown in Figure 1, carboxylate **2** has its P1 (*n*-butyl) and P2' (*p*-methoxybenzyl) residues extend-



Figure 1. Carboxylate **2** was cocrystallized in MMP-3.⁶ The figure shows the structure of carboxylate **2** extracted from the X-ray crystal structure (carbons are yellow with nitrogen blue and oxygen red).

ing toward solvent, away from the active site, where they become situated in close proximity to each other. This is a similar observation to that made in the previous paper for succinate hydroxamates.⁹ Thus, we surmised the P1 and P2' groups of an amino carboxylate could be connected to form a macrocycle of varying size. The solvent exposed area is large, and therefore we felt confident that the macrocycle, and various linking groups, would be accommodated there. Amino carboxylates orient themselves differently than the hydroxamates described in the previous paper,⁹ and this was taken into account in our modeling. This difference is manifested through the extra atom (nitrogen) in the extended conformation and a distinct mode of ligation to the active site zinc. From modeling, the larger ring amino carboxylates appeared to better preserve the extended conformation and the projection of the carboxylate to the active site zinc. To model this, the 14membered lactam 12 was docked into the active site of MMP-3. This orientation was refined with 20-ps of molecular dynamics using the procedure of Luty et al.¹⁰ Figure 2 shows the average structure during the final 3-ps of the run, which was overlapped with the crystal structure of carboxylate 2. This demonstrates that the macrocycle is a good mimic of the overall gross structure and provides for excellent overlap of the carboxylate moieties. Simulations were also carried out on lactam 12 within the active site of MMP-8.¹¹ The 3-ps average structure from the end of the run is displayed in Figure 3. This representation indicates that the lactam **12** is capable of participating in the typical hydrogen bond network well documented¹² for MMP inhibitors.

Synthesis. The macrocyclic amino carboxylates were synthesized by the representative route shown in Scheme

S0022-2623(97)00850-9 CCC: \$15.00 © 1998 American Chemical Society Published on Web 05/01/1998

[†] Inflammatory Diseases Research.

Table 1.



				$K_i (\mathbf{nM})^a$				
compd	п	W	R	MMP-1	MMP-2	MMP-3	MMP-8	MMP-9
13	linear			2860	1533	14088	293	404
11	1	$-CH_2-$	Ph	900	2400	35000	531	9800
12	2	$-CH_2-$	Ph	2500	8100	13500	17	6600
14	2	$-O_2CCH_2-$	Ph	8400	238	2900	10	5800
15	2	$-CH_2-$	PhPh	1448	249	2400	9	288

^{*a*} K_i's were determined as previously described.^{9,16}



Figure 2. Overlay between the minimized¹⁰ 14-membered lactam **12** (carbons are white with nitrogen blue and oxygen red) and carboxylate **2** from Figure 1 (carbons are yellow with nitrogen blue and oxygen red).

2 for carboxylate **11**. The aspartic acid derivative **3** was coupled to lysine **4** via a standard EDC coupling. The resulting amide **5** was treated with diethylamine to remove the Fmoc group and provide the primary amine **6**. In general, we found that amines of this type could be efficiently alkylated¹³ with triflate **7**¹⁴ to afford, in this case, the secondary amine **8**. Catalytic hydrogenation gave the amino acid **9**, which was cyclized under moderate dilution to yield the 13-membered lactam **10**. All that remained to complete the synthesis was removal of the *tert*-butyl group via TFA, thus providing the target macrocyclic amino carboxylate **11**.

Results and Discussion. The smallest macrocycle synthesized was the 13-membered lactam **11**, which displayed less affinity for MMP-2, -3, -8, and -9 when compared to the model, linear compound **13** (Table 1). As discussed above, the larger rings appeared superior from modeling, and therefore we synthesized the 14-membered lactam **12**. A 30-fold increase in activity



Figure 3. The minimized¹⁰ 14-membered lactam **12** (carbons are gray with nitrogen blue and oxygen red) docked into MMP-8 (carbons are white with nitrogen blue and oxygen red; catalytic zinc is orange).

toward MMP-8 was observed for **12** when compared to the 13-membered lactam **11**. In addition, the selectivity of **12** for MMP-8 was enhanced as compared to the other MMPs we screened. In keeping with this trend, we synthesized the 16-membered lactam **14**. Again, an increase in activity toward MMP-8 was observed for **14** versus the 14-membered lactam **12**. However, **14** was more potent against MMP-2, -3, and -9, and therefore less attractive than the selective **12**.

Another way to gain affinity in this class of inhibitors is to install biaryl groups in P1'.^{6,15} The resulting biaryl lactam **15** was only slightly more active toward MMP-8 than the parent **12**. The main limitation of the biaryl, however, is the enhanced affinity toward other MMPs with large S1' pockets. In fact, this was observed for **15**, as the inhibition of MMP-2, -3, and -9 increased dramatically. It is interesting to note that the biaryl had only a modest effect on MMP-1, known to have a restricted S1'.

Scheme 2^a



^{*a*} Reagents: (a) EDC, HOBt, NMM, L-Cbz-Lys-NHMe **4**, CH₂Cl₂ (47%); (b) Et₂NH, DMF (86%); (c) (*R*)-Ph(CH₂)₂(TfO)CHCO₂Bn **7**, *i*-Pr₂NEt, CH₂Cl₂, (78%); (d) H₂, Pd/C, MeOH; (e) BOP, *i*-Pr₂NEt, DMF (33%, two steps); (f) TFA, CH₂Cl₂ (95%).

Conclusion. In this communication, we demonstrated that linear, amino carboxylate MMP inhibitors can be transformed into macrocyclic inhibitors linked from P1 to P2'. We have discovered that ring size has an effect on activity, and that the larger rings were potent MMP-8 inhibitors. With the proper ring size and substituents, potent and selective MMP-8 inhibitors have been described. These unique structures should lead to a better understanding of ligand binding in the MMPs, as well as aid in the development of future inhibitors.

Supporting Information Available: Experimental details and spectroscopic data are available for the synthesis of compounds **5–11** (4 pages). Ordering information is given on any current masthead page.

References

- Current address: Department of Biochemistry and Biophysics, University of Pennsylvania School of Medicine, Philadelphia, PA 19104-6059.
- (2) For reviews, see: (a) Zask, A.; Levin, J. I.; Killar, L. M.; Skotnicki, J. S. Inhibition of Matrix Metalloproteinases: Structure Based Design. *Curr. Pharm. Des.* **1996**, *2*, 624–661. (b) Hagmann, W. K.; Lark, M. W.; Becker, J. W. Inhibition of Matrix Metalloproteinases. *Annu. Rep. Med. Chem.* **1996**, *31*, 231–240.
- (3) (a) Stetler-Stevenson W. G.; Krutzsch, H. C.; Liotta, L. A. Tissue Inhibitor of Metalloproteinase (TIMP-2): A New Member of the Metalloproteinase Family. *J. Biol. Chem.* **1989**, *264*, 17374– 17378. (b) Docherty, A. J. P.; Lyons, A.; Smith, B. J.; Wright, E.

M.; Stephens, P. E.; Harris, T. J. R.; Murphy, G.; Reynolds, J. J. Sequence of Human Tissue Inhibitor of Metalloproteinases and its Identity to Erythroid-Potentiating Activity. *Nature* **1985**, *318*, 66–69. (c) Enghold, J. J.; Salveson, G.; Brew, K.; Nagase, H. Interaction of Human Rheumatoid Synovial Collagenase (Matrix Metalloproteinase 1) and Stromelysin (Matrix Metalloproteinase 3) with Human α 2-Macroglobulin and Chicken Ovostatin. Binding Kinetics and Identification of Matrix Metalloproteinase Cleavage Sites. *J. Biol. Chem.* **1989**, *264*, 8779–8785.

- (4) (a) Sirum, K. L.; Brinckerhoff, C. E. Cloning of the Genes for Human Stromelysin and Stromelysin 2: Differential Expression in Rheumatoid Synovial Fibroblasts. *Biochemistry* **1989**, *28*, 8691–8698. (b) Gunja-Smith, Z.; Nagasse, H.; Woessner, J. F. Purification of the Neutral Proteoglycan-Degrading Metalloproteinase from Human Articular Cartilage Tissue and its Identification as Stromelysin Matrix Metalloproteinase-3. *Biochem. J.* **1989**, *258*, 115–119.
- (5) Rasmussen, H. S.; Hockel, G. M. Matrix Metalloproteinase Inhibition: A Potential New Anticancer Strategy. *Pharm. News* 1997, 4, 11–13.
- (6) Cherney, R. J.; Deciccio, C. P.; Nelson, D. J.; Wang, L.; Meyer, D. T.; Hardman, K. D.; Copeland, R. A.; Arner, E. C. Potent Carboxylate Inhibitors of Stromelysin Containing P2' Piperazic Acids and P1' Biaryl Moieties. *Bioorg. Med. Chem. Lett.* 1997, 7, 1757–1762.
- (7) Arner, E. C.; Decicco, C. P.; Cherney, R. J.; Tortorella, M. D. Cleavage of Native Cartilage Aggrecan by Neutrophil Collagenase (MMP-8) Is Distinct from Endogenous Cleavage by Aggrecanase. J. Biol. Chem. 1997, 272, 9294–9299.
- (8) The nomenclature for the MMPs discussed is as follows: MMP-1 (human fibroblast collagenase), MMP-2 (gelatinase A), MMP-3 (human fibroblast stromelysin), MMP-8 (human neutrophil collagenase), and MMP-9 (gelatinase B).
- (9) Xue, C.-B.; He, X.; Roderick, J.; Degrado, W. F.; Cherney, R. J.; Hardman, K. D.; Nelson, D. J.; Copeland, R. A.; Jaffee, B. D.; Decicco, C. P. Design and Synthesis of Cyclic Inhibitors of Matrix Metalloproteinases and TNF-α Production. J. Med. Chem. 1998, 41, 1745–1748.
- (10) Luty, B. A.; Wasserman, Z. R.; Stouten, P. F. W.; Hodge, C. N.; Zacharias, M.; McCammon, J. A. A Molecular Mechanics/grid Method for Evaluation of Ligand-Receptor Interactions. J. Comput. Chem. 1995, 16, 454-464.
- (11) The coordinates for MMP-8 were those of the following: Stams, T.; Spurlino, J. C.; Smith, D. L.; Wahl, R. C.; Ho, T. F.; Qoronfleh, M. W.; Banks, T. M.; Rubin, B. Structure of Human Neutrophil Collagenase Reveals Large S1' Specificity Pocket. *Nature Struct. Biol.* 1994, *1*, 119–123, Potein Data Bank File Imnc.
 (12) Dhanaraj, V.; Ye, Q.-Z.; Johnson, L. L.; Hupe, D. J.; Ortwine,
- (12) Dhanaraj, V.; Ye, Q.-Z.; Johnson, L. L.; Hupe, D. J.; Ortwine, D. F.; Dunbar, J. B.; Rubin, J. R.; Pavlovsky, A.; Humblet, C.; Blundell, T. L. X-ray Structure of a Hydroxamate Inhibitor Complex of Stromelysin Catalytic Domain and its Comparison with Members of the Zinc Metalloproteinase Superfamily. *Structure* **1996**, *4*, 375–386.
- (13) Kogan, T. P.; Somers, T. C.; Venuti, M. C. A Regio- and Stereocontrolled Total Synthesis of (-)-Indolactam-V. *Tetrahedron* 1990, 46, 6623–6632.
- (14) Triflate 7 was synthesized from the commercially available (Fluka) ethyl (*R*)-2-hydroxy-4-phenylbutyrate via the sequence:
 (a) LiOH, THF, H₂O.; (b) DBU, BnBr, PhH; (c) Tf₂O, 2,6-lutidine, CH₂Cl₂.
- (15) Esser, C. K.; Bugianesi, R. L.; Caldwell, C. G.; Chapman, K. T.; Durette, P. L.; Girotra, N. N.; Kopka, I. E.; Lanza, T. J.; Levorse, D. A.; MacCoss, M.; Owens, K. A.; Ponpipom, M. M.; Simeone, J. P.; Harrison, R. K.; Niedzwiecki, L.; Becker, J. W.; Marcy, A. I.; Axel, M. G.; Christen, A. J.; McDonnell, J.; Moore, V. L.; Olszewski, J. M.; Saphos, C.; Visco, D. M.; Shen, F.; Colletti, A.; Krieter, P. A.; Hagmann, W. K. Inhibition of Stromelysin-1 (MMP-3) by P1'-Biphenylylethyl Carboxyalkyl Dipeptides. J. Med. Chem. 1997, 40, 1026-1040.
- (16) Copeland, R. A.; Lombardo, D.; Giannaras, J.; Decicco, C. P. Estimating Ki Values for Tight Binding Inhibitors from Dose– Response Plots. *Bioorg. Med. Chem. Lett.* **1995**, *5*, 1947–1952.

JM970850Y